PF-0233-2 CON

NOVEL HUMAN CYTOKINE/STEROID RECEPTOR PROTEIN

This application is a continuation of a copending U.S. application Serial No. 09/203,548, filed December 1, 1998, which is a divisional application of U.S. application Serial No. 08/822,264, filed March 20, 1997, issued March 7, 2000, as U.S. Patent No. 6,033,869, entitled "Polynucleotide Encoding a Novel Human Cytokine/Steroid Receptor Protein," all of which are hereby expressly incorporated herein by reference.

FIELD OF THE INVENTION

This invention relates to nucleic acid and amino acid sequences of a novel cytokine/steroid receptor protein and to the use of these sequences in the diagnosis, prevention, and treatment of disorders associated with aberrant cellular development and differentiation and inflammation.

BACKGROUND OF THE INVENTION

2,3,7,8-Tetrachlorodibenzo-p-dioxin (TCDD; dioxin), an extremely potent rodent carcinogen, has also been shown to exhibit a wide spectrum of additional biological effects in a variety of species. These effects include alterations in metabolic pathways, developmental and reproductive changes, and immunotoxicity (Whitlock, J. (1994) Trends Endocrinol. Metab. 5:183-188; Hanson, C. and Smilalowicz, R. (1994) Toxicology 88:213-224). Despite extensive research, the molecular basis of dioxin toxicity remains poorly understood. Experimental evidence suggests that dioxin triggers its variety of biological responses by altering the expression of specific TCDD-responsive genes. This sequence of events is initiated when dioxin binds to the aromatic hydrocarbon receptor (Ah) and is followed by the interaction of the activated ligand-receptor complex with specific DNA response elements in the target genes. Among the TCDD-responsive genes are members of the P450 family, metabolic pathway enzymes, growth factor receptors including epidermal growth factor receptor, and several proteins associated with proinflammatory states such as interleukin 1B and plasminogen activator inhibitor 2 (Asman, D. et al. (1993) J. Biol. Chem. 268:12530-12536; Nebert, D. et al. (1991) Pharmacogenesis 1:68-78; and Sutter, T. et al.

(1991) Science 254:415-418). Although it is still highly speculative whether these genes are actively involved in carcinogenesis, it appears that dioxin may alter important cell cycle checkpoints in a variety of regulatory systems. Interestingly, estrogen treatment blocks the TCDD-induced accumulation of several of these gene products in MCF-7 breast cancer cells (Kharat, I. and

5   Saatcioglu, F. (1996) J. Biol. Chem. 271:10533-10537). Since TCDD has been shown to decrease estrogen-inducible gene products, it appears that two way cross-talk occurs between the intracellular signaling pathways involving steroids and aromatic hydrocarbons.

Using a PCR-based technique to identify differentially expressed genes, a novel cDNA called 25-Dx was isolated from rat livers exposed to TCDD (Selmin, O. et al. (1996)

10   Carcinogenesis 17:2609-2615). Expression of 25-Dx in liver was enhanced in a dose dependent fashion over a broad range of TCDD exposures. Northern analysis of untreated rat tissues demonstrated additional 25-Dx expression in brain, lung, kidney and normal liver. Expression of 25-Dx was low in testis and spleen and undetectable in heart and skeletal muscle.

The protein sequence of 25-Dx suggested its identification as a new member of the

15   cytokine/growth factor/prolactin receptor superfamily (Selmin et al., *supra*). The 25-Dx sequence contains a hydrophobic region which is 71% homologous to the transmembrane domain of the consensus IL-6 receptor sequence. In addition, an eight amino acid proline-rich region at amino acids 62 to 70 in the putative cytoplasmic domain of the 25-Dx protein is conserved within the receptor superfamily. This proline-rich region is necessary for the association of tyrosine kinases

20   with members of the cytokine/growth hormone/prolactin receptor superfamily. The 25-Dx sequence contains several tyrosine residues which provide potential phosphate acceptor sites during receptor activation. 25-Dx may thus be a mediator of a signal transduction pathway (Selmin et. al, *supra*). Furthermore, as TCDD exposure modulates immune and inflammatory responses, Selmin et al. (*supra*) propose that 25-Dx may play a role in TCDD immunotoxicity.

25   A cDNA sequence encoding a protein with a 76% amino acid homology to 25-Dx has been identified in porcine liver microsomes and vascular smooth muscle cells (Falkenstein, E. et al. (1996) Biochem. Biophys. Res. Commun. 229:86-89). The protein sequence encoded by this cDNA matches the N-terminal and internal CNBr fragments of a partially sequenced progesterone membrane binding protein isolated from porcine liver membranes (Meyer, C. et al. (1996) Eur. J.

Biochem. 239:726-731). Expression of this putative steroid membrane binding protein is tissue-specific and is similar to that observed for 25-Dx: high in brain, liver, lung and kidney, low in heart and spleen. Falkenstein et al. point out that this protein appears to be the first putative membrane-bound steroid receptor for which at least partial sequence data is available. Falkenstein et al.

5   propose that the progesterone binding protein may function in mediating rapid non-genomic steroid effects that are distinct from the known classic intracellular steroid receptor pathways (described in Fuller, P. (1991) FASEB J. 5:3092-3099).

The close identity of 25-Dx and the progesterone binding protein suggest a possible linkage between cytokine receptor-meditated signal transduction and steroid signaling pathways in the

10   development of both neoplastic and inflammatory responses. For example, a high level of internal homology exists among 25-Dx, the progesterone binding protein, and the transmembrane domain of the IL-6 receptor (Selmin et al., *supra* and Falkenstein et al., *supra*). The interaction of the IL-6 receptor with its cytokine is critical in polyclonal B-cell activation, and IL-6 levels are elevated in a number of inflammatory, autoimmune and malignant states including cervical carcinoma, lymphoma

15   and myeloma. Elevated IL-6 levels in transgenic mice result in massive plasmacytosis and mesangial proliferative glomerulonephritis. Interestingly, loss of an estrogen source as occurs in ovariectomy of mice produces an elevation in IL-6 levels and subsequent development of a osteoclastogenic osteoporosis (Narazaki, M. and Kishimoto, T. (1994) In: Nicola, N. (ed.) Guidebook to Cytokines and their Receptors, Oxford University Press, New York, NY, pp. 56-61).

20   Discovery of a new human cytokine/steroid receptor protein satisfies a need in the art by providing new compositions useful in diagnosing and treating disorders associated with aberrant cellular development and differentiation and inflammation.

25   **SUMMARY OF THE INVENTION**

The present invention features a novel cytokine/steroid receptor protein hereinafter designated CYSTAR and characterized as having similarity to the rat 25-Dx protein and the pig progesterone membrane binding protein.

Accordingly, the invention features a substantially purified CYSTAR having the amino acid sequence shown in SEQ ID NO:1.

One aspect of the invention features isolated and substantially purified polynucleotides that encode CYSTAR. In a particular aspect, the polynucleotide is the nucleotide sequence of SEQ ID

5   NO:2.

The invention also relates to a polynucleotide sequence comprising the complement of SEQ ID NO:2 or variants thereof. In addition, the invention features polynucleotide sequences which hybridize under stringent conditions to SEQ ID NO:2.

The invention additionally features nucleic acid sequences encoding polypeptides,

10   oligonucleotides, peptide nucleic acids (PNA), fragments, portions or antisense molecules thereof, and expression vectors and host cells comprising polynucleotides that encode CYSTAR. The present invention also features antibodies which bind specifically to CYSTAR, and pharmaceutical compositions comprising substantially purified CYSTAR. The invention also features agonists and antagonists of CYSTAR. The invention also features a method for producing CYSTAR. The

15   invention also features a method for treating disorders associated with aberrant cellular development by administering CYSTAR, and methods for treating disorders associated with differentiation and inflammation by administering antagonists of CYSTAR.

BRIEF DESCRIPTION OF THE FIGURES

20   Figures 1A, 1B, and 1C show the amino acid sequence (SEQ ID NO:1) and nucleic acid sequence (SEQ ID NO:2) of CYSTAR. The alignment was produced using MACDNASIS PRO software (Hitachi Software Engineering Co., Ltd., San Bruno, CA).

Figures 2A and 2B show the amino acid sequence alignments among CYSTAR (SEQ ID NO:1), rat 25-Dx protein (GI 1518818; SEQ ID NO:3) and pig progesterone membrane binding

25   protein (GI 1657409; SEQ ID NO:4). The alignment was produced using the multisequence alignment program of DNASTAR software (DNASTAR Inc, Madison WI).

Figures 3A and 3B show the hydrophobicity plots (MACDNASIS PRO software) for CYSTAR (SEQ ID NO: 1), and 25-Dx protein (SEQ ID NO:3), respectively. The positive X axis reflects amino acid position, and the negative Y axis, hydrophobicity.

4

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular methodology, protocols, cell lines, vectors, and reagents described as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to "a host cell" includes a plurality of such host cells, reference to the "antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods, devices, and materials are now described. All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are reported in the publications which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"Nucleic acid sequence", as used herein, refers to an oligonucleotide, nucleotide, or polynucleotide, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin which may be single- or double-stranded, and represent the sense or antisense strand. Similarly, "amino acid sequence", as used herein, refers to an oligopeptide, peptide, polypeptide, or protein sequence, and fragments or portions thereof, and to naturally occurring or synthetic molecules.

Where "amino acid sequence" is recited herein to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms, such as "polypeptide" or "protein" are not meant to limit the amino acid sequence to the complete, native amino acid sequence associated with the recited protein molecule.

5   "Peptide nucleic acid", as used herein, refers to a molecule which comprises an oligomer to which an amino acid residue, such as lysine, and an amino group have been added. These small molecules, also designated anti-gene agents, stop transcript elongation by binding to their complementary strand of nucleic acid (Nielsen, P.E. et al. (1993) Anticancer Drug Des. 8:53-63).

CYSTAR, as used herein, refers to the amino acid sequences of substantially purified

10   CYSTAR obtained from any species, particularly mammalian, including bovine, ovine, porcine, murine, equine, and preferably human, from any source whether natural, synthetic, semi-synthetic, or recombinant.

"Consensus", as used herein, refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, or which has been extended using the XL-PCR kit (Perkin Elmer,

15   Norwalk, CT) in the 5' and/or the 3' direction and resequenced, or which has been assembled from the overlapping sequences of more than one Incyte clone using the GELVIEW fragment assembly system (GCG, Madison, WI), or which has been both extended and assembled.

A "variant" of CYSTAR, as used herein, refers to an amino acid sequence that is altered by one or more amino acids. The variant may have "conservative" changes, wherein a substituted

20   amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. More rarely, a variant may have "nonconservative" changes, e.g., replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known

25   in the art, for example, DNASTAR software.

A "deletion", as used herein, refers to a change in either amino acid or nucleotide sequence in which one or more amino acid or nucleotide residues, respectively, are absent.

An "insertion" or "addition", as used herein, refers to a change in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid or nucleotide residues, respectively, as compared to the naturally occurring molecule.

A "substitution", as used herein, refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

The term "biologically active", as used herein, refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic CYSTAR, or any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "agonist", as used herein, refers to a molecule which, when bound to CYSTAR, increases the amount of, or prolongs the duration of, the activity of CYSTAR. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to CYSTAR.

The term "antagonist", as used herein, refers to a molecule which, when bound to CYSTAR, decreases the biological or immunological activity of CYSTAR. Antagonists and inhibitors may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to CYSTAR.

The term "modulate", as used herein, refers to a change or an alteration in the biological activity of CYSTAR. Modulation may be an increase or a decrease in protein activity, a change in binding characteristics, or any other change in the biological, functional or immunological properties of CYSTAR.

The term "mimetic", as used herein, refers to a molecule, the structure of which is developed from knowledge of the structure of CYSTAR or portions thereof and, as such, is able to effect some or all of the actions of cytokine/steroid receptor-like molecules.

The term "derivative", as used herein, refers to the chemical modification of a nucleic acid encoding CYSTAR or the encoded CYSTAR. Illustrative of such modifications would be replacement of hydrogen by an alkyl, acyl, or amino group. A nucleic acid derivative would encode a polypeptide which retains essential biological characteristics of the natural molecule.

7

The term "substantially purified", as used herein, refers to nucleic or amino acid sequences that are removed from their natural environment, isolated or separated, and are at least 60% free, preferably 75% free, and most preferably 90% free from other components with which they are naturally associated.

5   "Amplification," as used herein, refers to the production of additional copies of a nucleic acid sequence and is generally carried out using polymerase chain reaction (PCR) technologies well known in the art (Dieffenbach, C.W. and G.S. Dveksler (1995) PCR Primer, a Laboratory Manual, Cold Spring Harbor Press, Plainview, NY).

The term "hybridization", as used herein, refers to any process by which a strand of nucleic
10   acid binds with a complementary strand through base pairing.

The term "hybridization complex", as used herein, refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary G and C bases and between complementary A and T bases; these hydrogen bonds may be further stabilized by base stacking interactions. The two complementary nucleic acid sequences hydrogen
15   bond in an antiparallel configuration. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., membranes, filters, chips, pins or glass slides to which cells have been fixed for in situ hybridization).

The terms "complementary" or "complementarity", as used herein, refer to the natural
20   binding of polynucleotides under permissive salt and temperature conditions by base-pairing. For example, the sequence "A-G-T" binds to the complementary sequence "T-C-A". Complementarity between two single-stranded molecules may be "partial", in which only some of the nucleic acids bind, or it may be complete when total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on
25   the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands.

The term "homology", as used herein, refers to a degree of complementarity. There may be partial homology or complete homology (i.e., identity). A partially complementary sequence is one that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid; it is

8

referred to using the functional term "substantially homologous." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or probe will compete for and inhibit the

5 binding (i.e., the hybridization) of a completely homologous sequence or probe to the target sequence under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require that the binding of two sequences to one another be a specific (i.e., selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of

10 complementarity (e.g., less than about 30% identity); in the absence of non-specific binding, the probe will not hybridize to the second non-complementary target sequence.

As known in the art, numerous equivalent conditions may be employed to comprise either low or high stringency conditions. Factors such as the length and nature (DNA, RNA, base composition) of the sequence, nature of the target (DNA, RNA, base composition, presence in

15 solution or immobilization, etc.), and the concentration of the salts and other components (e.g., the presence or absence of formamide, dextran sulfate and/or polyethylene glycol) are considered and the hybridization solution may be varied to generate conditions of either low or high stringency different from, but equivalent to, the above listed conditions.

The term "stringent conditions", as used herein, is the "stringency" which occurs within a

20 range from about Tm-5°C (5°C below the melting temperature (Tm) of the probe) to about 20°C to 25°C below Tm. As will be understood by those of skill in the art, the stringency of hybridization may be altered in order to identify or detect identical or related polynucleotide sequences.

The term "antisense", as used herein, refers to nucleotide sequences which are complementary to a specific DNA or RNA sequence. The term "antisense strand" is used in

25 reference to a nucleic acid strand that is complementary to the "sense" strand. Antisense molecules may be produced by any method, including synthesis by ligating the gene(s) of interest in a reverse orientation to a viral promoter which permits the synthesis of a complementary strand. Once introduced into a cell, this transcribed strand combines with natural sequences produced by the cell to form duplexes. These duplexes then block either the further transcription or translation. In this

9

manner, mutant phenotypes may be generated. The designation "negative" is sometimes used in reference to the antisense strand, and "positive" is sometimes used in reference to the sense strand.

The term "portion", as used herein, with regard to a protein (as in "a portion of a given protein") refers to fragments of that protein. The fragments may range in size from four amino acid

5   residues to the entire amino acid sequence minus one amino acid. Thus, a protein "comprising at least a portion of the amino acid sequence of SEQ ID NO:1" encompasses the full-length human CYSTAR and fragments thereof.

"Transformation", as defined herein, describes a process by which exogenous DNA enters and changes a recipient cell. It may occur under natural or artificial conditions using various

10   methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed and may include, but is not limited to, viral infection, electroporation, lipofection, and particle bombardment. Such "transformed" cells include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously

15   replicating plasmid or as part of the host chromosome. They also include cells which transiently express the inserted DNA or RNA for limited periods of time.

The term "antigenic determinant", as used herein, refers to that portion of a molecule that makes contact with a particular antibody (i.e., an epitope). When a protein or fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of

20   antibodies which bind specifically to a given region or three-dimensional structure on the protein; these regions or structures are referred to as antigenic determinants. An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The terms "specific binding" or "specifically binding", as used herein, in reference to the

25   interaction of an antibody and a protein or peptide, mean that the interaction is dependent upon the presence of a particular structure (i.e., the antigenic determinant or epitope) on the protein; in other words, the antibody is recognizing and binding to a specific protein structure rather than to proteins in general. For example, if an antibody is specific for epitope "A", the presence of a protein

containing epitope A (or free, unlabeled A) in a reaction containing labeled "A" and the antibody will reduce the amount of labeled A bound to the antibody.

The term "sample", as used herein, is used in its broadest sense. A biological sample suspected of containing nucleic acid encoding CYSTAR or fragments thereof may comprise a cell,

5   chromosomes isolated from a cell (e.g., a spread of metaphase chromosomes), genomic DNA (in solution or bound to a solid support such as for Southern analysis), RNA (in solution or bound to a solid support such as for northern analysis), cDNA (in solution or bound to a solid support), an extract from cells or a tissue, and the like.

The term "correlates with expression of a polynucleotide", as used herein, indicates that the

10   detection of the presence of ribonucleic acid that is similar to SEQ ID NO:2 by northern analysis is indicative of the presence of mRNA encoding CYSTAR in a sample and thereby correlates with expression of the transcript from the polynucleotide encoding the protein.

"Alterations" in the polynucleotide of SEQ ID NO:2, as used herein, comprise any alteration in the sequence of polynucleotides encoding CYSTAR including deletions, insertions, and

15   point mutations that may be detected using hybridization assays. Included within this definition is the detection of alterations to the genomic DNA sequence which encodes CYSTAR (e.g., by alterations in the pattern of restriction fragment length polymorphisms capable of hybridizing to SEQ ID NO:2), the inability of a selected fragment of SEQ ID NO:2 to hybridize to a sample of genomic DNA (e.g., using allele-specific oligonucleotide probes), and improper or unexpected hybridization,

20   such as hybridization to a locus other than the normal chromosomal locus for the polynucleotide sequence encoding CYSTAR (e.g., using fluorescent in situ hybridization (FISH) to metaphase chromosome spreads).

As used herein, the term "antibody" refers to intact molecules as well as fragments thereof, such as Fa, F(ab')$_2$, and Fv, which are capable of binding the epitopic determinant. Antibodies that

25   bind CYSTAR polypeptides can be prepared using intact polypeptides or fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an animal can be derived from the transition of RNA or synthesized chemically, and can be conjugated to a carrier protein, if desired. Commonly used carriers that are chemically coupled to

peptides include bovine serum albumin and thyroglobulin. The coupled peptide is then used to immunize the animal (e.g., a mouse, a rat, or a rabbit).

The term "humanized antibody", as used herein, refers to antibody molecules in which amino acids have been replaced in the non-antigen binding regions in order to more closely

5   resemble a human antibody, while still retaining the original binding ability.

THE INVENTION

The invention is based on the discovery of a novel human cytokine/steroid receptor protein (CYSTAR), the polynucleotides encoding CYSTAR, and the use of these compositions for the

10   diagnosis, prevention, or treatment of disorders associated with aberrant cellular development and differentiation including cancers and inflammation.

Nucleic acids encoding the human CYSTAR of the present invention were first identified in Incyte Clone 2504333 from the mesentery tumor cDNA library (CONUTUT01) through a computer-generated search for amino acid sequence alignments. A consensus sequence, SEQ ID

15   NO:2, was derived from the following overlapping and/or extended nucleic acid sequences: Incyte Clones 311917 (LUNGNOT02); 1438826 (PANCNOT08); 2240970 (PANTUT02); and 2504333 (CONUTUT01).

In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:1, as shown in Figures 1A, 1B, and 1C. CYSTAR is 220 amino acids in

20   length and has chemical and structural homology (Figures 2A and 2B) with rat 25-Dx protein (GI 1518818; SEQ ID NO:3) and porcine steroid membrane binding protein (GI 1657409; SEQ ID NO:4). In particular, CYSTAR shares 79% identity with rat 25-Dx protein and 93% identity with porcine steroid membrane binding protein. As illustrated by Figures 3A and 3B, CYSTAR and rat 25-Dx protein have similar hydrophobicity plots. CYSTAR contains a potential transmembrane

25   domain extending approximately from positions 18 to 43 of SEQ ID NO:1. CYSTAR contains potential casein kinase II (positions 74, 152, 154, 181), protein kinase C (positions 161, 190, 191), and tyrosine kinase (position 172) phosphorylation sites on the C-terminal side of the predicted transmembrane domain. Northern analysis shows the expression of CYSTAR in nervous, secretory, urinary, endocrine, reproductive tract and gastrointestinal tissues, including

brain, spinal cord, fibroblasts, adrenal gland, liver, lung, bladder, colon, small intestine, kidney, prostate, breast, pancreas, and pituitary. Many of these tissues are associated with tumors or inflammation. Of particular note is the expression of CYSTAR in fetal and infant brain, lung, and liver/spleen, which suggests a developmental role for this molecule.

5   The invention also encompasses CYSTAR variants. A preferred CYSTAR variant is one having at least 80%, and more preferably 90%, amino acid sequence identity to the CYSTAR amino acid sequence (SEQ ID NO:1). A most preferred CYSTAR variant is one having at least 95% amino acid sequence identity to SEQ ID NO:1.

        The invention also encompasses polynucleotides which encode CYSTAR. Accordingly,

10   any nucleic acid sequence which encodes the amino acid sequence of CYSTAR can be used to generate recombinant molecules which express CYSTAR. In a particular embodiment, the invention encompasses the polynucleotide comprising the nucleic acid sequence of SEQ ID NO:2 as shown in Figures 1A, 1B and 1C.

        It will be appreciated by those skilled in the art that as a result of the degeneracy of the

15   genetic code, a multitude of nucleotide sequences encoding CYSTAR, some bearing minimal homology to the nucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of nucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the

20   nucleotide sequence of naturally occurring CYSTAR, and all such variations are to be considered as being specifically disclosed.

        Although nucleotide sequences which encode CYSTAR and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring CYSTAR under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide

25   sequences encoding CYSTAR or its derivatives possessing a substantially different codon usage. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding CYSTAR and its derivatives without altering the encoded amino acid sequences include

the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences, or portions thereof, which encode CYSTAR and its derivatives, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents that are well known in the art at the time of the filing of this application. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding CYSTAR or any portion thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed nucleotide sequences, and in particular, those shown in SEQ ID NO:2, under various conditions of stringency. Hybridization conditions are based on the melting temperature (Tm) of the nucleic acid binding complex or probe, as taught in Wahl, G.M. and S.L. Berger (1987; Methods Enzymol. 152:399-407) and Kimmel, A.R. (1987; Methods Enzymol. 152:507-511), and may be used at a defined stringency.

Altered nucleic acid sequences encoding CYSTAR which are encompassed by the invention include deletions, insertions, or substitutions of different nucleotides resulting in a polynucleotide that encodes the same or a functionally equivalent CYSTAR. The encoded protein may also contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent CYSTAR. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the biological activity of CYSTAR is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid; positively charged amino acids may include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; phenylalanine and tyrosine.

Also included within the scope of the present invention are alleles of the genes encoding CYSTAR. As used herein, an "allele" or "allelic sequence" is an alternative form of the gene which may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene

may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

5   Methods for DNA sequencing which are well known and generally available in the art may be used to practice any embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical Corp, Cleveland, OH), Taq polymerase (Perkin Elmer), thermostable T7 polymerase (Amersham, Chicago, IL), or combinations of recombinant polymerases and proofreading exonucleases such as the ELONGASE

10   amplification system marketed by Gibco BRL (Gaithersburg, MD). Preferably, the process is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno, NV), PTC200 thermal cycler (MJ Research, Watertown, MA) and the ABI 377 DNA sequencers (Perkin Elmer).

      The nucleic acid sequences encoding CYSTAR may be extended utilizing a partial

15   nucleotide sequence and employing various methods known in the art to detect upstream sequences such as promoters and regulatory elements. For example, one method which may be employed, "restriction-site" PCR, uses universal primers to retrieve unknown sequence adjacent to a known locus (Sarkar, G. (1993) PCR Methods Applic. 2:318-322). In particular, genomic DNA is first amplified in the presence of primer to linker sequence and a primer specific to the known region.

20   The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

      Inverse PCR may also be used to amplify or extend sequences using divergent primers based on a known region (Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186). The primers may

25   be designed using OLIGO 4.06 primer analysis software (National Biosciences Inc., Plymouth, MN), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

· Another method which may be used is capture PCR which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119). In this method, multiple restriction enzyme digestions and ligations may also be used to place an engineered double-stranded

5   sequence into an unknown portion of the DNA molecule before performing PCR.

Another method which may be used to retrieve unknown sequences is that of Parker, J.D. et al. (1991; Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries to walk in genomic DNA (Clontech, Palo Alto, CA). This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

10   When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Also, random-primed libraries are preferable, in that they will contain more sequences which contain the 5' regions of genes. Use of a randomly primed library may be especially preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into the 5' and 3' non-transcribed

15   regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths

20   by a charge coupled device camera. Output/light intensity may be converted to electrical signal using appropriate software (e.g. GENOTYPER and SEQUENCE NAVIGATOR, Perkin Elmer) and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA which might be present in limited amounts in a particular sample.

25   In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode CYSTAR, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of CYSTAR in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the

same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express CYSTAR.

As will be understood by those of skill in the art, it may be advantageous to produce CYSTAR-encoding nucleotide sequences possessing non-naturally occurring codons. For

5 example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

The nucleotide sequences of the present invention can be engineered using methods

10 generally known in the art in order to alter CYSTAR encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns,

15 change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding CYSTAR may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of CYSTAR activity, it may be useful to encode a chimeric CYSTAR protein that can be recognized by a commercially available

20 antibody. A fusion protein may also be engineered to contain a cleavage site located between the CYSTAR encoding sequence and the heterologous protein sequence, so that CYSTAR may be cleaved and purified away from the heterologous moiety.

In another embodiment, sequences encoding CYSTAR may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M.H. et al. (1980) Nucl. Acids

25 Res. Symp. Ser. 215-223, Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of CYSTAR, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J.Y. et al. (1995) Science 269:202-204)

and automated synthesis may be achieved, for example, using the ABI 431A peptide synthesizer (Perkin Elmer).

The newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) Proteins, Structures and Molecular

5   Principles, WH Freeman and Co., New York, NY). The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure; Creighton, *supra*). Additionally, the amino acid sequence of CYSTAR, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

10   In order to express a biologically active CYSTAR, the nucleotide sequences encoding CYSTAR or functional equivalents, may be inserted into appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence.

Methods which are well known to those skilled in the art may be used to construct

15   expression vectors containing sequences encoding CYSTAR and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. Such techniques are described in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, NY, and Ausubel, F.M. et al. (1989) Current Protocols in Molecular Biology, John

20   Wiley & Sons, New York, NY.

A variety of expression vector/host systems may be utilized to contain and express sequences encoding CYSTAR. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus

25   expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular

proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the

5   BLUESCRIPT phagemid (Stratagene, LaJolla, CA) or PSPORT1 plasmid (Gibco BRL) and the like may be used. The baculovirus polyhedrin promoter may be used in insect cells. Promoters or enhancers derived from the genomes of plant cells (e.g., heat shock, RUBISCO; and storage protein genes) or from plant viruses (e.g., viral promoters or leader sequences) may be cloned into the vector. In mammalian cell systems, promoters from mammalian genes or from mammalian

10   viruses are preferable. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding CYSTAR, vectors based on SV40 or EBV may be used with an appropriate selectable marker.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for CYSTAR. For example, when large quantities of CYSTAR are needed for the

15   induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional E. coli cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding CYSTAR may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of ß-galactosidase so that a hybrid protein is produced; pIN vectors

20   (Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509); and the like. pGEX vectors (Promega, Madison, WI) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include

25   heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, Saccharomyces cerevisiae, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (*supra*) and Grant et al. (1987) Methods Enzymol. 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding CYSTAR may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters

5   such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L.E. in

10   McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, NY; pp. 191-196).

An insect system may also be used to express CYSTAR. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in Spodoptera frugiperda cells or in Trichoplusia larvae. The sequences encoding

15   CYSTAR may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of CYSTAR will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, S. frugiperda cells or Trichoplusia larvae in which CYSTAR may be expressed (Engelhard, E.K. et al. (1994) Proc. Nat. Acad. Sci. 91:3224-3227).

20   In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding CYSTAR may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing CYSTAR in infected host cells (Logan,

25   J. and Shenk, T. (1984) Proc. Natl. Acad. Sci. 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding CYSTAR. Such signals include the ATG initiation codon and adjacent sequences. In

cases where sequences encoding CYSTAR, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be

5   provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) Results Probl. Cell Differ. 20:125-162).

10   In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different

15   host cells such as CHO, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express CYSTAR may be transformed using

20   expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the

25   introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) Cell 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1980) Cell 22:817-23)

21

genes which can be employed in tk⁻ or aprt⁻ cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al

5 (1981) J. Mol. Biol. 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. 85:8047-51). Recently, the use of visible markers has gained

10 popularity with such markers as anthocyanins, ß glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C.A. et al. (1995) Methods Mol. Biol. 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest

15 is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding CYSTAR is inserted within a marker gene sequence, recombinant cells containing sequences encoding CYSTAR can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding CYSTAR under the control of a single promoter. Expression of the marker gene in response to induction or

20 selection usually indicates expression of the tandem gene as well.

Alternatively, host cells which contain the nucleic acid sequence encoding CYSTAR and express CYSTAR may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include membrane, solution, or chip based

25 technologies for the detection and/or quantification of nucleic acid or protein.

The presence of polynucleotide sequences encoding CYSTAR can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or portions or fragments of polynucleotides encoding CYSTAR. Nucleic acid amplification based assays involve the use of oligonucleotides or oligomers based on the sequences encoding CYSTAR to detect transformants

22

containing DNA or RNA encoding CYSTAR. As used herein "oligonucleotides" or "oligomers" refer to a nucleic acid sequence of at least about 10 nucleotides and as many as about 60 nucleotides, preferably about 15 to 30 nucleotides, and more preferably about 20-25 nucleotides, which can be used as a probe or amplimer.

5   A variety of protocols for detecting and measuring the expression of CYSTAR, using either polyclonal or monoclonal antibodies specific for the protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on CYSTAR is preferred, but a competitive

10   binding assay may be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul, MN) and Maddox, D.E. et al. (1983; J. Exp. Med. 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled

15   hybridization or PCR probes for detecting sequences related to polynucleotides encoding CYSTAR include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding CYSTAR, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA

20   polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits (Pharmacia & Upjohn, (Kalamazoo, MI); Promega (Madison WI); and U.S. Biochemical Corp., (Cleveland, OH)). Suitable reporter molecules or labels, which may be used, include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

25   Host cells transformed with nucleotide sequences encoding CYSTAR may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CYSTAR may be designed to contain signal

sequences which direct secretion of CYSTAR through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding CYSTAR to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as

5   histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, WA). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, CA) between the purification domain and CYSTAR may be used to facilitate purification. One such

10   expression vector provides for expression of a fusion protein containing CYSTAR and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, Prot. Exp. Purif. 3: 263-281) while the enterokinase cleavage site provides a means for purifying CYSTAR from the fusion protein. A discussion of vectors

15   which contain fusion proteins is provided in Kroll, D.J. et al. (1993; DNA Cell Biol. 12:441-453).

In addition to recombinant production, fragments of CYSTAR may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) J. Am. Chem. Soc. 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using the AB1 431A peptide synthesizer

20   (Perkin Elmer). Various fragments of CYSTAR may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

THERAPEUTICS

Chemical and structural homology exists among CYSTAR, 25-Dx protein from rat, and

25   progesterone membrane binding protein from pig. Furthermore, CYSTAR is expressed in nervous, secretory, urinary, endocrine, reproductive tract and gastrointestinal tissues, many of which are associated with tumors or inflammation. CYSTAR therefore appears to play a role in cellular development and differentiation and in inflammation.

Therefore, in one embodiment, CYSTAR or a fragment or derivative thereof may be administered to a subject to treat a developmental disorder. Such disorders may include, but are not limited to, spina bifida, hydrocephalus, achondroplastic dwarfism, renal tubular acidosis, anemia, gonadal dysgenesis, congenital glaucoma or cataract, congenital sensorineural hearing loss, seizure

5   disorders such as Syndenham's chorea and cerebral palsy, epilepsy, cerebrovascular disease induced by ischemic or hypertensive disease, and hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis.

In another embodiment, a vector capable of expressing CYSTAR, or a fragment or derivative thereof, may also be administered to a subject to treat or prevent a developmental

10   disorder, including those listed above.

In another embodiment, antagonists of CYSTAR may be administered to a subject to treat or prevent a disorder associated with aberrant cellular differentiation. Such disorders may include, but are not limited to: hyperaldosteronism (Conn's Syndrome), hypocortisolism (Addison's disease), hypercortisolism (Cushing's disease), and adrenogenital syndrome, and cancers, including

15   cancers of the nervous system, cancers of glands, tissues, and organs involved in secretion or absorption such as prostate, lung, bladder, adrenal gland, liver, uterus, and kidney, and cancers of tissues of the immune and hematopoietic systems. In one aspect, antibodies which are specific for CYSTAR may be used directly as an antagonist, or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express CYSTAR.

20   In another embodiment, a vector expressing the complementary or antisense sequence of the polynucleotide encoding CYSTAR may be administered to a subject to treat or prevent a disorder associated with aberrant cellular differentiation including those listed above.

In another embodiment, antagonists of CYSTAR may be administered to a subject to treat or prevent inflammation. Inflammation may be associated with, but is not limited to, allergic

25   reactions, asthma and adult respiratory distress syndrome, rheumatoid arthritis, osteoarthritis, glomerulonephritis, osteoporosis, dermatomyositis, polymyositis, Addison's disease, Grave's disease, irritable bowel syndrome, atrophic gastritis, lupus erythematosus, myasthenia gravis, multiple sclerosis, autoimmune thyroiditis, ulcerative colitis, anemia, pancreatitis, scleroderma, Crohn's disease, ischemia/reperfusion injury, post-traumatic inflammation, myocardial inflammation,

25

atherosclerosis, multiple sclerosis, and inflammatory complications of cancer, hemodialysis and extracorporeal circulation, infection and trauma. In one aspect, antibodies which are specific for CYSTAR may be used directly as an antagonist, or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express CYSTAR.

In another embodiment, a vector expressing the complementary or antisense sequence of the polynucleotide encoding CYSTAR may be administered to a subject to treat or prevent inflammation associated with expression of CYSTAR, including those conditions listed above.

In other embodiments, any of the therapeutic proteins, antagonists, antibodies, agonists, antisense sequences or vectors described above may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

Antagonists or inhibitors of CYSTAR may be produced using methods which are generally known in the art. In particular, purified CYSTAR may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind CYSTAR.

Antibodies specific for CYSTAR may be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies, (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others, may be immunized by injection with CYSTAR or any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol.

Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and <u>Corynebacterium</u> <u>parvum</u> are especially preferable.

It is preferred that the peptides, fragments, or oligopeptides used to induce antibodies to CYSTAR have an amino acid sequence consisting of at least five amino acids, and more preferably

5   at least 10 amino acids. It is also preferable that they are identical to a portion of the amino acid sequence of the natural protein, and they may contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of CYSTAR amino acids may be fused with those of another protein such as keyhole limpet hemocyanin and antibody produced against the chimeric molecule.

10   Monoclonal antibodies to CYSTAR may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. 80:2026-2030; Cole,

15   S.P. et al. (1984) Mol. Cell Biol. 62:109-120).

In addition, techniques developed for the production of "chimeric antibodies", the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity can be used (Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; Takeda, S. et al. (1985)

20   Nature 314:452-454). Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce CYSTAR-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries (Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. 88:11120-11123).

25   Antibodies may also be produced by inducing <u>in</u> <u>vivo</u> production in the lymphocyte population or by screening recombinant immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. 86: 3833-3837; Winter, G. et al. (1991) Nature 349:293-299).

Antibody fragments which contain specific binding sites for CYSTAR may also be generated. For example, such fragments include, but are not limited to, the $F(ab')_2$ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragments. Alternatively, Fab expression

5 libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse, W.D. et al. (1989) Science 254:1275-1281).

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such

10 immunoassays typically involve the measurement of complex formation between CYSTAR and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering CYSTAR epitopes is preferred, but a competitive binding assay may also be employed (Maddox, *supra*).

In another embodiment of the invention, the polynucleotides encoding CYSTAR, or any

15 fragment thereof, or antisense molecules, may be used for therapeutic purposes. In one aspect, antisense to the polynucleotide encoding CYSTAR may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding CYSTAR. Thus, antisense molecules may be used to modulate CYSTAR activity, or to achieve regulation of gene function. Such technology

20 is now well known in the art, and sense or antisense oligomers or larger fragments, can be designed from various locations along the coding or control regions of sequences encoding CYSTAR.

Expression vectors derived from retroviruses, adenovirus, herpes or vaccinia viruses, or from various bacterial plasmids may be used for delivery of nucleotide sequences to the targeted organ, tissue or cell population. Methods which are well known to those skilled in the art can be

25 used to construct recombinant vectors which will express antisense molecules complementary to the polynucleotides of the gene encoding CYSTAR. These techniques are described both in Sambrook et al. (*supra*) and in Ausubel et al. (*supra*).

Genes encoding CYSTAR can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide or fragment thereof which encodes CYSTAR.

28

Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell.
Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA
molecules until they are disabled by endogenous nucleases. Transient expression may last for a
month or more with a non-replicating vector and even longer if appropriate replication elements are
5   part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing
antisense molecules, DNA, RNA, or PNA, to the control regions of the gene encoding CYSTAR,
i.e., the promoters, enhancers, and introns. Oligonucleotides derived from the transcription initiation
site, e.g., between positions -10 and +10 from the start site, are preferred. Similarly, inhibition can
10   be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it
causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases,
transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have
been described in the literature (Gee, J.E. et al. (1994) In: Huber, B.E. and B.I. Carr, <u>Molecular</u>
<u>and</u> <u>Immunologic</u> <u>Approaches</u>, Futura Publishing Co., Mt. Kisco, NY). The antisense molecules
15   may also be designed to block translation of mRNA by preventing the transcript from binding to
ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage
of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the
ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage.
20   Examples which may be used include engineered hammerhead motif ribozyme molecules that can
specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding CYSTAR.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by
scanning the target molecule for ribozyme cleavage sites which include the following sequences:
GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20
25   ribonucleotides corresponding to the region of the target gene containing the cleavage site may be
evaluated for secondary structural features which may render the oligonucleotide inoperable. The
suitability of candidate targets may also be evaluated by testing accessibility to hybridization with
complementary oligonucleotides using ribonuclease protection assays.

Antisense molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding

5   CYSTAR. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize antisense RNA constitutively or inducibly can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible

10   modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of

15   adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same

20   patient. Delivery by transfection and by liposome injections may be achieved using methods which are well known in the art.

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

25   An additional embodiment of the invention relates to the administration of a pharmaceutical composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of CYSTAR, antibodies to CYSTAR, mimetics, agonists, antagonists, or inhibitors of CYSTAR. The compositions may be administered alone or in combination with at least one other agent, such as stabilizing compound,

30

which may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing Co., Easton, PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures.

Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol.

5   Push-fit capsules can contain active ingredients mixed with a filler or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in

10   aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or

15   synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

20   The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc.

25   Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1-50 mM histidine, 0.1%-2% sucrose, and 2-7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of CYSTAR, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models, usually mice, rabbits, dogs, or pigs. The animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example CYSTAR or fragments thereof, antibodies of CYSTAR, agonists, antagonists or inhibitors of CYSTAR, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., ED50 (the dose therapeutically effective in 50% of the population) and LD50 (the dose lethal to 50% of the population). The dose ratio of toxic to therapeutic effects is the therapeutic index, and it can be expressed as the ratio, LD50/ED50. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject that requires treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions may be administered

33

every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and

5   methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

10   **DIAGNOSTICS**

In another embodiment, antibodies which specifically bind CYSTAR may be used for the diagnosis of conditions or diseases characterized by expression of CYSTAR, or in assays to monitor patients being treated with CYSTAR, agonists, antagonists or inhibitors. The antibodies useful for diagnostic purposes may be prepared in the same manner as those described above for

15   therapeutics. Diagnostic assays for CYSTAR include methods which utilize the antibody and a label to detect CYSTAR in human body fluids or extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by joining them, either covalently or non-covalently, with a reporter molecule. A wide variety of reporter molecules which are known in the art may be used, several of which are described above.

20   A variety of protocols including ELISA, RIA, and FACS for measuring CYSTAR are known in the art and provide a basis for diagnosing altered or abnormal levels of CYSTAR expression. Normal or standard values for CYSTAR expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to CYSTAR under conditions suitable for complex formation. The amount of standard complex

25   formation may be quantified by various methods, but preferably by photometric means. Quantities of CYSTAR expressed in subject samples, control and disease, from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding CYSTAR may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, antisense RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of CYSTAR may be

5   correlated with disease. The diagnostic assay may be used to distinguish between absence, presence, and excess expression of CYSTAR, and to monitor regulation of CYSTAR levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding CYSTAR or closely related

10   molecules, may be used to identify nucleic acid sequences which encode CYSTAR. The specificity of the probe, whether it is made from a highly specific region, e.g., 10 unique nucleotides in the 5' regulatory region, or a less specific region, e.g., especially in the 3' coding region, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low) will determine whether the probe identifies only naturally occurring sequences encoding CYSTAR, alleles, or related

15   sequences.

Probes may also be used for the detection of related sequences, and should preferably contain at least 50% of the nucleotides from any of the CYSTAR encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and derived from the nucleotide sequence of SEQ ID NO:2 or from genomic sequence including promoter, enhancer elements, and

20   introns of the naturally occurring CYSTAR.

Means for producing specific hybridization probes for DNAs encoding CYSTAR include the cloning of nucleic acid sequences encoding CYSTAR or CYSTAR derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA

25   polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, radionuclides such as 32P or 35S, or enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding CYSTAR may be used for the diagnosis of disorders or inflammation associated with expression of CYSTAR. Examples of such disorders or conditions

include spina bifida, hydrocephalus, achondroplastic dwarfism, renal tubular acidosis, anemia, gonadal dysgenesis, congenital glaucoma or cataract, congenital sensorineural hearing loss, Syndenham's chorea, cerebral palsy, epilepsy, cerebrovascular disease induced by ischemic or hypertensive disease, hereditary neuropathies such as Charcot-Marie-Tooth disease and

5   neurofibromatosis, hyperaldosteronism (Conn's Syndrome), hypocortisolism (Addison's disease), hypercortisolism (Cushing's disease), adrenogenital syndrome, cancers of the nervous system, cancers of glands, tissues, and organs involved in secretion or absorption such as prostate, lung, bladder, adrenal gland, liver, uterus, and kidney, and cancers of tissues of the immune and hematopoietic systems, allergic reactions, asthma and adult respiratory distress syndrome,

10   rheumatoid arthritis, osteoarthritis, glomerulonephritis, osteoporosis, dermatomyositis, polymyositis, Addison's disease, Grave's disease, irritable bowel syndrome, atrophic gastritis, lupus erythematosus, myasthenia gravis, multiple sclerosis, autoimmune thyroiditis, ulcerative colitis, anemia, pancreatitis, scleroderma, Crohn's disease, ischemia/reperfusion injury, post-traumatic inflammation, myocardial inflammation, atherosclerosis, multiple sclerosis, and inflammatory

15   complications of cancer, hemodialysis and extracorporeal circulation, infection and trauma. The polynucleotide sequences encoding CYSTAR may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; or in dip stick, pin, ELISA or chip assays utilizing fluids or tissues from patient biopsies to detect altered CYSTAR expression. Such qualitative or quantitative methods are well known in the art.

20   In a particular aspect, the nucleotide sequences encoding CYSTAR may be useful in assays that detect activation or induction of various cancers, particularly those mentioned above. The nucleotide sequences encoding CYSTAR may be labeled by standard methods, and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated

25   and compared with a standard value. If the amount of signal in the biopsied or extracted sample is significantly altered from that of a comparable control sample, the nucleotide sequences have hybridized with nucleotide sequences in the sample, and the presence of altered levels of nucleotide sequences encoding CYSTAR in the sample indicates the presence of the associated disease. Such

36

assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or in monitoring the treatment of an individual patient.

In order to provide a basis for the diagnosis of disease associated with expression of CYSTAR, a normal or standard profile for expression is established. This may be accomplished by

5   combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, which encodes CYSTAR, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with those from an experiment where a known amount of a substantially purified polynucleotide is used. Standard values obtained from normal samples may be

10   compared with values obtained from samples from patients who are symptomatic for disease. Deviation between standard and subject values is used to establish the presence of disease.

Once disease is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to evaluate whether the level of expression in the patient begins to approximate that which is observed in the normal patient. The results obtained from successive

15   assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more

20   definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding CYSTAR may involve the use of PCR. Such oligomers may be chemically synthesized, generated

25   enzymatically, or produced from a recombinant source. Oligomers will preferably consist of two nucleotide sequences, one with sense orientation (5'->3') and another with antisense (3'<-5'), employed under optimized conditions for identification of a specific gene or condition. The same two oligomers, nested sets of oligomers, or even a degenerate pool of oligomers may be employed

under less stringent conditions for detection and/or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantitate the expression of CYSTAR include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and standard

5 curves onto which the experimental results are interpolated (Melby, P.C. et al. (1993) J. Immunol. Methods, 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 229-236). The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

10 In another embodiment of the invention, the nucleic acid sequences which encode CYSTAR may also be used to generate hybridization probes which are useful for mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome or to a specific region of the chromosome using well known techniques. Such techniques include FISH, FACS, or artificial chromosome constructions, such as yeast artificial chromosomes,

15 bacterial artificial chromosomes, bacterial P1 constructions or single chromosome cDNA libraries as reviewed in Price, C.M. (1993) Blood Rev. 7:127-134, and Trask, B.J. (1991) Trends Genet. 7:149-154.

FISH (as described in Verma et al. (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York, NY) may be correlated with other physical chromosome

20 mapping techniques and genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of the gene encoding CYSTAR on a physical chromosomal map and a specific disease, or predisposition to a specific disease, may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between

25 normal, carrier, or affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques such as linkage analysis using established chromosomal markers may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not

known. New sequences can be assigned to chromosomal arms, or parts thereof, by physical

mapping. This provides valuable information to investigators searching for disease genes using

positional cloning or other gene discovery techniques. Once the disease or syndrome has been

crudely localized by genetic linkage to a particular genomic region, for example, AT to 11q22-23

5   (Gatti, R.A. et al. (1988) Nature 336:577-580), any sequences mapping to that area may represent

associated or regulatory genes for further investigation. The nucleotide sequence of the subject

invention may also be used to detect differences in the chromosomal location due to translocation,

inversion, etc. among normal, carrier, or affected individuals.

In another embodiment of the invention, CYSTAR, its catalytic or immunogenic fragments

10   or oligopeptides thereof, can be used for screening libraries of compounds in any of a variety of

drug screening techniques. The fragment employed in such screening may be free in solution,

affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of

binding complexes, between CYSTAR and the agent being tested, may be measured.

Another technique for drug screening which may be used provides for high throughput

15   screening of compounds having suitable binding affinity to the protein of interest as described in

published PCT application WO84/03564. In this method, as applied to CYSTAR, large numbers

of different small test compounds are synthesized on a solid substrate, such as plastic pins or some

other surface. The test compounds are reacted with CYSTAR, or fragments thereof, and washed.

Bound CYSTAR is then detected by methods well known in the art. Purified CYSTAR can also

20   be coated directly onto plates for use in the aforementioned drug screening techniques.

Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a

solid support.

In another embodiment, one may use competitive drug screening assays in which

neutralizing antibodies capable of binding CYSTAR specifically compete with a test compound for

25   binding CYSTAR. In this manner, the antibodies can be used to detect the presence of any peptide

which shares one or more antigenic determinants with CYSTAR.

In additional embodiments, the nucleotide sequences which encode CYSTAR may be used

in any molecular biology techniques that have yet to be developed, provided the new techniques

rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

The examples below are provided to illustrate the subject invention and are not included for the purpose of limiting the invention.

5

EXAMPLES

I   CONUTUT01 cDNA Library Construction

The CONUTUT01 cDNA library was constructed from sigmoid mesentery tumor tissue removed from a 61-year old female during abdominal excision of multiple tumors. Pathology

10   indicated a metastatic grade 4 malignant mixed mullerian tumor present in the sigmoid mesentery at two sites. Pathology of adjacent tissues indicated a grade 4 malignant mixed Mullerian tumor, heterologous type of the uterus forming a firm, infiltrating mass throughout the myometrium and involving the serosal surface. The heterologous elements of the tumor consisted of rhabdomyoblasts and immature cartilage. The tumor also involved the lower uterine segment and extended into the

15   cervical wall. Extensive lymphatic and vascular permeation was identified in the myometrium and cervical wall. A single (of 7) right common iliac and a single (of 7) right external iliac lymph nodes were identified with metastatic grade 4 malignant mixed mullerian tumor with the metastases comprised mainly of adenocarcinoma. Estrogen and progesterone receptor studies were positive.

The frozen tissue was homogenized and lysed in Trizol reagent (1 gm tissue/10 ml Trizol;

20   Gibco/BRL, Gaithersburg, MD), a monoplastic solution of phenol and guanidine isothiocyanate, using a Brinkmann POLYTRON PT-3000 homogenizer (Brinkmann Instruments, Westbury, NY). After a brief incubation on ice, chloroform was added (1:5 v/v), and the lysate was centrifuged. The upper chloroform layer was removed to a fresh tube, and the RNA extracted with isopropanol, resuspended in DEPC-treated water, and DNase treated for 25 min at 37°C. The RNA was re-

25   extracted twice with acid phenol-chloroform pH 4.7 and precipitated using 0.3M sodium acetate and 2.5 volumes ethanol. The mRNA was isolated with the OLIGOTEX kit (QIAGEN, Inc., Chatsworth, CA) and used to construct the cDNA library.

The mRNA was handled according to the recommended protocols in the SUPERSCRIPT plasmid system. CONUTUT01 cDNAs were fractionated on a SEPHAROSE CL4B column, and

those cDNAs exceeding 400 bp were ligated into pINCY 1. The plasmid pINCY 1 was subsequently transformed into DH5α competent cells.

II   Isolation and Sequencing of cDNA Clones

5   Plasmid DNA was released from the cells and purified using the R.E.A.L. PREP 96 plasmid kit (QIAGEN, Inc.). The recommended protocol was employed except for the following changes: 1) the bacteria were cultured in 1 ml of sterile Terrific Broth (GIBCO/BRL) with carbenicillin at 25 mg/L and glycerol at 0.4%; 2) after inoculation, the cultures were incubated for 19 hours and at the end of incubation, the cells were lysed with 0.3 ml of lysis buffer; and 3)

10   following isopropanol precipitation, the plasmid DNA pellet was resuspended in 0.1 ml of distilled water. After the last step in the protocol, samples were transferred to a 96-well block for storage at 4° C.

The cDNAs were sequenced by the method of Sanger et al. (1975, J. Mol. Biol. 94:441f), using a MICROLAB 2200 liquid transfer system (Hamilton, Reno, NV) in combination with

15   PTC200 thermal cyclers (MJ Research, Watertown, MA) and AB1 377 DNA sequencing systems (Perkin Elmer); and the reading frame was determined.

III   Homology Searching of cDNA Clones and Their Deduced Proteins

The nucleotide sequences of the Sequence Listing or amino acid sequences deduced from

20   them were used as query sequences against databases such as GenBank, SwissProt, BLOCKS, and Pima II. These databases which contain previously identified and annotated sequences were searched for regions of homology (similarity) using BLAST, which stands for Basic Local Alignment Search Tool (Altschul, S.F. (1993) J. Mol. Evol. 36:290-300; Altschul et al. (1990) J. Mol. Biol. 215:403-410).

25   BLAST produces alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST is especially useful in determining exact matches or in identifying homologs which may be of prokaryotic (bacterial) or eukaryotic (animal, fungal or plant) origin. Other algorithms such as the one described in Smith, R.F. and T.F. Smith (1992; Protein Engineering 5:35-51), incorporated herein by reference, can be

used when dealing with primary sequence patterns and secondary structure gap penalties. As disclosed in this application, the sequences have lengths of at least 49 nucleotides, and no more than 12% uncalled bases (where N is recorded rather than A, C, G, or T).

The BLAST approach, as detailed in Karlin, S. and S.F. Altschul (1993; Proc. Nat.

5   Acad. Sci. 90:5873-7) and incorporated herein by reference, searches for matches between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. In this application, threshold was set at 10^{-25} for nucleotides and 10^{-14} for peptides.

Incyte nucleotide sequences were searched against the GenBank databases for primate

10   (pri), rodent (rod), and mammalian sequences (mam), and deduced amino acid sequences from the same clones are searched against GenBank functional protein databases, mammalian (mamp), vertebrate (vrtp) and eukaryote (eukp), for homology. The relevant database for a particular match were reported as a GIxxx±p (where xxx is pri, rod, etc and if present, p = peptide).

15   **IV   Northern Analysis**

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound (Sambrook et al., *supra*).

Analogous computer techniques using BLAST (Altschul, S.F. 1993 and 1990, *supra*) are

20   used to search for identical or related molecules in nucleotide databases such as GenBank or the LIFESEQ database (Incyte Pharmaceuticals). This analysis is much faster than multiple, membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or homologous.

The basis of the search is the product score which is defined as:

25
$$\frac{\text{\% sequence identity x \% maximum BLAST score}}{100}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1-2% error; and at 70, the match will be exact. Homologous molecules are usually

42

identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analysis are reported as a list of libraries in which the transcript encoding CYSTAR occurs. Abundance and percent abundance are also reported. Abundance

5   directly reflects the number of times a particular transcript is represented in a cDNA library, and percent abundance is abundance divided by the total number of sequences examined in the cDNA library.

V   Extension of CYSTAR-Encoding Polynucleotides

10   Nucleic acid sequence from Incyte clone 2504333 or SEQ ID NO:2 is used to design oligonucleotide primers for extending a partial nucleotide sequence to full length or for obtaining 5' or 3', intron or other control sequences from genomic libraries. One primer is synthesized to initiate extension in the antisense direction (XLR) and the other is synthesized to extend sequence in the sense direction (XLF). Primers are used to facilitate the extension of the known sequence

15   "outward" generating amplicons containing new, unknown nucleotide sequence for the region of interest. The initial primers are designed from the cDNA using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations

20   is avoided.

The original, selected cDNA libraries, or a human genomic library are used to extend the sequence; the latter is most useful to obtain 5' upstream regions. If more extension is necessary or desired, additional sets of primers are designed to further extend the known region.

By following the instructions for the XL-PCR kit (Perkin Elmer) and thoroughly mixing the

25   enzyme and reaction mix, high fidelity amplification is obtained. Beginning with 40 pmol of each primer and the recommended concentrations of all other components of the kit, PCR is performed using the PTC200 thermal cycler (M.J. Research, Watertown, MA) and the following parameters:

Step 1   94° C for 1 min (initial denaturation)

Step 2	65° C for 1 min
Step 3	68° C for 6 min
Step 4	94° C for 15 sec
Step 5	65° C for 1 min
Step 6	68° C for 7 min
Step 7	Repeat step 4-6 for 15 additional cycles
Step 8	94° C for 15 sec
Step 9	65° C for 1 min
Step 10	68° C for 7:15 min
Step 11	Repeat step 8-10 for 12 cycles
Step 12	72° C for 8 min
Step 13	4° C (and holding)

A 5-10 μl aliquot of the reaction mixture is analyzed by electrophoresis on a low concentration (about 0.6-0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. Bands thought to contain the largest products are selected and removed from the gel. Further purification involves using a commercial gel extraction method such as QIAQUICK (QIAGEN Inc., Chatsworth, CA). After recovery of the DNA, Klenow enzyme is used to trim single-stranded, nucleotide overhangs creating blunt ends which facilitate religation and cloning.

After ethanol precipitation, the products are redissolved in 13 μl of ligation buffer, 1μl T4-DNA ligase (15 units) and 1μl T4 polynucleotide kinase are added, and the mixture is incubated at room temperature for 2-3 hours or overnight at 16° C. Competent E. coli cells (in 40 μl of appropriate media) are transformed with 3 μl of ligation mixture and cultured in 80 μl of SOC medium (Sambrook et al., *supra*). After incubation for one hour at 37° C, the whole transformation mixture is plated on Luria Bertani (LB)-agar (Sambrook et al., *supra*) containing 2x Carb. The following day, several colonies are randomly picked from each plate and cultured in 150 μl of liquid LB/2x Carb medium placed in an individual well of an appropriate, commercially-available, sterile 96-well microtiter plate. The following day, 5 μl of each overnight culture is transferred into a non-sterile 96-well plate and after dilution 1:10 with water, 5 μl of each sample is transferred into a PCR array.

For PCR amplification, 18 μl of concentrated PCR reaction mix (3.3x) containing 4 units of rTth DNA polymerase, a vector primer, and one or both of the gene specific primers used for the

extension reaction are added to each well. Amplification is performed using the following

conditions:

Step 1	94° C for 60 sec
Step 2	94° C for 20 sec
Step 3	55° C for 30 sec
Step 4	72° C for 90 sec
Step 5	Repeat steps 2-4 for an additional 29 cycles
Step 6	72° C for 180 sec
Step 7	4° C (and holding)

Aliquots of the PCR reactions are run on agarose gels together with molecular weight

markers. The sizes of the PCR products are compared to the original partial cDNAs, and

appropriate clones are selected, ligated into plasmid, and sequenced.

VI   Labeling and Use of Hybridization Probes

Hybridization probes derived from SEQ ID NO:2 are employed to screen cDNAs,

genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20

base-pairs, is specifically described, essentially the same procedure is used with larger cDNA

fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06

(National Biosciences), labeled by combining 50 pmol of each oligomer and 250 μCi of [γ-^{32}P]

adenosine triphosphate (Amersham) and T4 polynucleotide kinase (DuPont NEN, Boston, MA).

The labeled oligonucleotides are substantially purified with a SEPHADEX G-25 superfine resin

column (Pharmacia & Upjohn). A portion containing 10^7 counts per minute of each of the sense

and antisense oligonucleotides is used in a typical membrane based hybridization analysis of human

genomic DNA digested with one of the following endonucleases (Ase I, Bgl II, Eco RI, Pst I, Xba

1, or Pvu II; DuPont NEN).

The DNA from each digest is fractionated on a 0.7 percent agarose gel and transferred to

nylon membranes (Nytran Plus, Schleicher & Schuell, Durham, NH). Hybridization is carried out

for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room

temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5%

sodium dodecyl sulfate. After XOMAT AR film (Kodak, Rochester, NY) is exposed to the blots

in a PHOSPHOIMAGER cassette (Molecular Dynamics, Sunnyvale, CA) for several hours,

hybridization patterns are compared visually.

5   **VII   Antisense Molecules**

Antisense molecules or nucleic acid sequence complementary to the CYSTAR-encoding

sequence, or any part thereof, is used to inhibit in vivo or in vitro expression of naturally occurring

CYSTAR. Although use of antisense oligonucleotides, comprising about 20 base-pairs, is

specifically described, essentially the same procedure is used with larger cDNA fragments. An

10   oligonucleotide based on the coding sequences of CYSTAR, as shown in Figures 1A, 1B, and 1C,

is used to inhibit expression of naturally occurring CYSTAR. The complementary oligonucleotide is

designed from the most unique 5' sequence as shown in Figures 1A, 1B, and 1C and used either to

inhibit transcription by preventing promoter binding to the upstream nontranslated sequence or

translation of an CYSTAR-encoding transcript by preventing the ribosome from binding. Using an

15   appropriate portion of the signal and 5' sequence of SEQ ID NO:2, an effective antisense

oligonucleotide includes any 15-20 nucleotides spanning the region which translates into the signal

or 5' coding sequence of the polypeptide as shown in Figures 1A, 1B, and 1C.

VIII   Expression of CYSTAR

20   Expression of CYSTAR is accomplished by subcloning the cDNAs into appropriate

vectors and transforming the vectors into host cells. In this case, the cloning vector, PSPORT1,

previously used for the generation of the cDNA library is used to express CYSTAR in E. coli.

Upstream of the cloning site, this vector contains a promoter for ß-galactosidase, followed by

sequence containing the amino-terminal Met, and the subsequent seven residues of ß-galactosidase.

25   Immediately following these eight residues is a bacteriophage promoter useful for transcription and a

linker containing a number of unique restriction sites.

Induction of an isolated, transformed bacterial strain with IPTG using standard methods

produces a fusion protein which consists of the first eight residues of ß-galactosidase, about 5 to 15

residues of linker, and the full length protein. The signal residues direct the secretion of CYSTAR into the bacterial growth media which can be used directly in the following assay for activity.

IX   Demonstration of CYSTAR Activity

5   CYSTAR can be expressed in an immortalized mammalian cell line such as MEQC by transforming the cells with a eukaryotic expression vector encoding CYSTAR. Eukaryotic expression vectors are commercially available, and the techniques to introduce them into cells are well known to those skilled in the art. A small amount of a second plasmid, which expresses any one of a number of reporter genes such as ß-galactosidase, is co-transformed into the cells in order

10   to allow rapid identification of those cells which have taken up and expressed the foreign DNA. The cells are cocultured with NIH 3T3 cells in a defined synthetic medium with increasing concentrations of TCDD for at least 48 hours after transformation to allow expression and accumulation of CYSTAR and ß-galactosidase.

Transformed cells expressing ß-galactosidase are stained blue when a suitable colorimetric

15   substrate is added to the culture media under conditions that are well known in the art. Increasing concentrations of TCDD produce increasing numbers of reporter gene positive cells as the expression of CYSTAR is induced (Selmin, O. et al., *supra*). TCDD-treated cells which were not transformed with the CYSTAR expression vector prior to 3T3 coculture are used as controls and tested in parallel.

20

X   Production of CYSTAR Specific Antibodies

CYSTAR that is substantially purified using PAGE electrophoresis (Sambrook, *supra*), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols. The amino acid sequence deduced from SEQ ID NO:2 is analyzed using DNASTAR

25   software (DNASTAR Inc) to determine regions of high immunogenicity and a corresponding oligopolypeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions, is described by Ausubel et al. (*supra*), and others.

Typically, the oligopeptides are 15 residues in length, synthesized using an AB1 431A

peptide synthesizer (Perkin Elmer) using fmoc-chemistry, and coupled to keyhole limpet

hemocyanin (KLH, Sigma, St. Louis, MO) by reaction with N-maleimidobenzoyl-N-

hydroxysuccinimide ester (MBS; Ausubel et al., *supra*). Rabbits are immunized with the

5   oligopeptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for

antipeptide activity, for example, by binding the peptide to plastic, blocking with 1% BSA, reacting

with rabbit antisera, washing, and reacting with radioiodinated, goat anti-rabbit IgG.

XI   Purification of Naturally Occurring CYSTAR Using Specific Antibodies

10   Naturally occurring or recombinant CYSTAR is substantially purified by immunoaffinity

chromatography using antibodies specific for CYSTAR. An immunoaffinity column is constructed

by covalently coupling CYSTAR antibody to an activated chromatographic resin, such as

CNBr-activated SEPHAROSE (Pharmacia & Upjohn). After the coupling, the resin is blocked

and washed according to the manufacturer's instructions.

15   Media containing CYSTAR is passed over the immunoaffinity column, and the column is

washed under conditions that allow the preferential absorbance of CYSTAR (e.g., high ionic

strength buffers in the presence of detergent). The column is eluted under conditions that disrupt

antibody/CYSTAR binding (eg, a buffer of pH 2-3 or a high concentration of a chaotrope, such as

urea or thiocyanate ion), and CYSTAR is collected.

20

XII   Identification of Molecules Which Interact with CYSTAR

CYSTAR or biologically active fragments thereof are labeled with ^{125}I Bolton-Hunter

reagent (Bolton et al. (1973) Biochem. J. 133: 529). Candidate molecules previously arrayed in

the wells of a multi-well plate are incubated with the labeled CYSTAR, washed and any wells with

25   labeled CYSTAR complex are assayed. Data obtained using different concentrations of CYSTAR

are used to calculate values for the number, affinity, and association of CYSTAR with the candidate

molecules.

All publications and patents mentioned in the above specification are herein incorporated

by reference. Various modifications and variations of the described method and system of the

invention will be apparent to those skilled in the art without departing from the scope and spirit of

the invention. Although the invention has been described in connection with specific preferred

embodiments, it should be understood that the invention as claimed should not be unduly limited to

such specific embodiments. Indeed, various modifications of the described modes for carrying out

5 the invention which are obvious to those skilled in molecular biology or related fields are intended to

be within the scope of the following claims.